In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 9, lines 9-17 and replace it with the following paragraph:

Figure 2 is a diagrammatic representation of the TaBV genomic region, from which the TaBV promoter fragments were derived. Positions and sequences of a region resembling the CaMV 35S promoter as-1 element and of putative TATA box and $tRNA^{met}$ binding site are indicated by dash lines. The predicted position of open reading frame 1 (ORF 1) and ORF 3 are also indicated. All promoter fragments within bracket A were created with restriction sites as indicated by labeled boxes, except for the *XbaI* site which exists within the native TaBV sequence. Promoter fragments within bracket B were generated by directional cloning of fragments in bracket A, as indicated by grey arrows using indicated restriction sites. Promoter fragment T600L was generated by removal of the *Pst* I/*Xba* I fragment from T1200L and, in the process, destroying the *Xba* I site **(SEQ ID NOS 31-33 disclosed respectively in order of appearance)**.

Please delete the paragraph on page 25, line 31 to page 26, line 5 and replace it with the following paragraph:

The TaBV genomic sequence comprises three ORF's, which encode the amino acid sequences set forth in SEQ ID NO: 3, 4 and 5, respectively. Sequence comparisons between these ORFs and the ORFs of other badnaviruses including those of BSV, ComYMV, CSSV, CYMV, DaBV and SCBV, showed sequences identities ranging from 20-37% for ORF 1, 13-23% for ORF 2 and 30-37% for ORF 3. ORF 3 showed most similarly to that of other badnaviruses due to the presence of conserved motifs common to other badnaviruses including movement motifs, the RNA-binding domain (RB; C-X2-C-X4-H-X4-C) **(SEQ ID NO: 30)** the second cysteine rich sequence (CYS) of unknown function, the aspartic protease motifs, reverse transcriptase domains and RNase H domains.